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# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Schlessinger, Joseph  
Sap, Jan M.
- (ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
PHOSPHATASE-ALPHA
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: PENNIE & EDMONDS
  - (B) STREET: 1155 AVENUE OF THE AMERICAS
  - (C) CITY: NEW YORK
  - (D) STATE: NEW YORK
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/015,985
  - (B) FILING DATE: 10-FEB-1993
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Coruzzi, Laura A.
  - (B) REGISTRATION NUMBER: 30,742
  - (C) REFERENCE/DOCKET NUMBER: 7683-020
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (212) 790-9090
  - (B) TELEFAX: (212) 869-9741/8864
  - (C) TELEX: 66141 PENNIE

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 802 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys
 1           5           10           15
Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr
 20           25           30
Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Glu Ala Lys
 35           40           45
Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr
 50           55           60
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Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn  
 65 70 75 80  
 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser  
 85 90 95  
 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln  
 100 105 110  
 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala  
 115 120 125  
 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys  
 130 135 140  
 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser  
 145 150 155 160  
 Ser Leu Leu Val Ile Val Phe Ile Ile Ile Val Leu Tyr Met Leu Arg  
 165 170 175  
 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu  
 180 185 190  
 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu  
 195 200 205  
 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp  
 210 215 220  
 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu  
 225 230 235 240  
 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr  
 245 250 255  
 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val  
 260 265 270  
 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu  
 275 280 285  
 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr  
 290 295 300  
 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr  
 305 310 315 320  
 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile  
 325 330 335  
 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln  
 340 345 350  
 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser  
 355 360 365  
 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys  
 370 375 380  
 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile  
 385 390 395 400  
 Thr Gln Phe His Phe Thr Ser Trp Pro Asp Phe Gly Val Pro Phe Thr  
 405 410 415  
 Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Ala Cys Asn Pro

420	425	430
Gln Tyr Ala Gly Ala Ile Val Val His Cys Ser Ala Gly Val Gly Arg 435 440 445		
Thr Gly Thr Phe Val Val Ile Asp Ala Met Leu Asp Met Met His Thr 450 455 460		
Glu Arg Lys Val Asp Val Tyr Gly Phe Val Ser Arg Ile Arg Ala Gln 465 470 475 480		
Arg Cys Gln Met Val Gln Thr Asp Met Gln Tyr Val Phe Ile Tyr Gln 485 490 495		
Ala Leu Leu Glu His Tyr Leu Tyr Gly Asp Thr Glu Leu Glu Val Thr 500 505 510		
Ser Leu Glu Thr His Leu Gln Lys Ile Tyr Asn Lys Ile Pro Gly Thr 515 520 525		
Ser Asn Asn Gly Leu Glu Glu Glu Phe Lys Lys Leu Thr Ser Ile Lys 530 535 540		
Ile Gln Asn Asp Lys Met Arg Thr Gly Asn Leu Pro Ala Asn Met Lys 545 550 555 560		
Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn Arg Val Ile 565 570 575		
Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val Asn Ala Ser 580 585 590		
Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala Ser Gln Gly 595 600 605		
Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile Trp Glu Trp 610 615 620		
Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu Arg Gly Gln 625 630 635 640		
Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val Ser Tyr Gly 645 650 655		
Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu Ser Tyr Thr 660 665 670		
Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys Ser Arg Gln 675 680 685		
Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ser 690 695 700		
Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln Lys Gln Gln 705 710 715 720		
Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala 725 730 735		
Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu Glu Arg Val 740 745 750		
Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys Ser Leu Arg 755 760 765		
Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys 770 775 780		

Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn  
785 790 795 800

Phe Lys

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2409 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGATTCTTCT GGTTCATTCT TGTTCGTCTC GGCAGTGGTC TGATATGTGT CAGTGCCAAC	60
AATGCTACCA CAGTTGCACC TTCTGTAGGA ATTACAAGAT TAATTAAGTC ATCAACGGCA	120
GAACCAAGTTA AAGAAGAGGC CAAACTTCA AATCCAAGTT CTTCACTAAC TTCTCTTTCT	180
GTGGCACCAA CATTACAGCC AAATATAACT CTGGGACCCA CCTATTTAAC CACTGTCAAT	240
TCTTCAGACT CTGACAATGG GACCACAAGA ACAGCAAGCA CCAATTCTAT AGGCATTACA	300
ATTTACCAA ATGGAACGTG GCTTCCAGAT AACCAGTTCA CGGATGCCAG AACAGAACCC	360
TGGGAGGGGA ATTCCAGCAC CGCAGCAACC ACTCCAGAAA CTTTCCCTCC TTCAGGTAAT	420
TCTGACTCGA AGGACAGAAG AGATGAGACA CCAATTATTG CGGTGATGGT GGCCCTGTCC	480
TCTCTGCTAG TGATCGTGTT TATTATCATA GTTTTGTACA TGTTAAGGTT TAAGAAATAC	540
AAGCAAGCTG GGAGCCATTC CAATTCTTTC CGCTTATCCA ACGGCCGCAC TGAGGATGTG	600
GAGCCCCAGA GTGTGCCACT TCTGGCCAGA TCCCCAAGCA CCAACAGGAA ATACCCACCC	660
CTGCCCCGTGG ACAAGCTGGA AGAGGAAATT AACCAGGAGAA TGGCAGACGA CAATAAGCTC	720
TTCAGGGAGG AATTCAACGC TCTCCCTGCA TGTCCTATCC AGGCCACCTG TGAGGCTGCT	780
TCCAAGGAGG AAAACAAGGA AAAAATCGA TATGTAAACA TCTTGCCTTA TGACCACTCT	840
AGAGTCCACC TGACACCGGT TGAAGGGGTT CCAGATTCTG ATTACATCAA TGCTTCATTC	900
ATCAACGGTT ACCAAGAAAA GAACAAATTC ATTGCTGCAC AAGGACCAA AGAAGAAACG	960
GTGAATGATT TCTGGCGGAT GATCTGGGAA CAAACACAG CCACCATCGT CATGGTTACC	1020
AACCTGAAGG AGAGAAAGGA GTGCAAGTGC GCCCAGTACT GGCCAGACCA AGGCTGCTGG	1080
ACCTATGGGA ATATTCGGGT GTCTGTAGAG GATGTGACTG TCCTGGTGGA CTACACAGTA	1140
CGGAAGTTCT GCATCCAGCA GGTGGGCGAC ATGACCAACA GAAAGCCACA GCGCCTCATC	1200
ACTCAGTTCC ACTTTACCAG CTGGCCAGAC TTTGGGGTGC CTTTACCCC GATCGGCATG	1260
CTCAAGTTCC TCAAGAAGGT GAAGGCCTGT AACCTCAGT ATGCAGGGGC CATCGTGGTC	1320
CACTGCAGTG CAGGTGTAGG GCGTACAGGT ACCTTTGTCTG TCATTGATGC CATGCTGGAC	1380
ATGATGCATA CAGAACGGAA GGTGGACGTG TATGGCTTTG TGAGCCGGAT CCGGGCACAG	1440
CGCTGCCAGA TGGTGCAAAC CGATATGCAG TATGTCTTCA TATACCAAGC CCTTCTGGAG	1500

CATTATCTCT ATGGAGATAC AGAACTGGAA GTGACCTCTC TAGAAACCCA CCTGCAGAAA 1560  
 ATTTACAACA AAATCCCAGG GACCAGCAAC AATGGATTAG AGGAGGAGTT TAAGAAGTTA 1620  
 ACATCAATCA AAATCCAGAA TGACAAGATG CGGACTGGAA ACCTTCCAGC CAACATGAAG 1680  
 AAGAACCGTG TTTTACAGAT CATTCCATAT GAATTCAACA GAGTGATCAT TCCAGTTAAG 1740  
 CGGGGCGAAG AGAATACAGA CTATGTGAAC GCATCCTTTA TTGATGGCTA CCGGCAGAAG 1800  
 GACTCCTATA TCGCCAGOCA GGGCCCTCTT CTCCACACAA TTGAGGACTT CTGGCGAATG 1860  
 ATCTGGGAGT GGAAATCCTG CTCTATCGTG ATGCTAACAG AACTGGAGGA GAGAGGCCAG 1920  
 GAGAAGTGTG CCCAGTACTG GCCATCTGAT GGAAGTGGTGT CCTATGGAGA TATTACAGTG 1980  
 GAACTGAAGA AGGAGGAGGA ATGTGAGAGC TACACCGTCC GAGACCTCCT GGTCACCAAC 2040  
 ACCAGGGAGA ATAAGAGCCG GCAGATCCGG CAGTTCCACT TCCATGGCTG GCCTGAAGTG 2100  
 GGCATCCCCA GTGACGGAAA GGGCATGATC AGCATCATCG CCGCCGTGCA GAAGCAGCAG 2160  
 CAGCAGTCAG GGAACCACCC CATCACCGTG CACTGCAGCG CCGGGGCAGG AAGGACGGGG 2220  
 ACCTTCTGTG CCCTGAGCAC CGTCCTGGAG CGTGTGAAAG CAGAGGGGAT TTTGGATGTC 2280  
 TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG 2340  
 TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC 2400  
 TTCAAGTAA 2409

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His  
 1 5 10 15  
 Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr  
 20 25 30  
 Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys  
 35 40 45  
 Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr  
 50 55 60  
 Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn  
 65 70 75 80  
 Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser  
 85 90 95  
 Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln  
 100 105 110  
 Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala  
 115 120 125

Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile  
130 135 140

Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile  
145 150 155 160

Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser  
165 170 175

His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu  
180 185 190

Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys  
195 200 205

Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg  
210 215 220

Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro  
225 230 235 240

Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn  
245 250 255

Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg  
260 265 270

Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn  
275 280 285

Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala  
290 295 300

Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp  
305 310 315 320

Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu Arg  
325 330 335

Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Cys Trp Thr  
340 345 350

Tyr Gly Asn Val Arg Val Ser Val Glu Asp Val Thr Val Leu Val Asp  
355 360 365

Tyr Thr Val Arg Lys Phe Ser Ile Gln Gln Val Gly Asp Val Thr Asn  
370 375 380

Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp Pro  
385 390 395 400

Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu Lys  
405 410 415

Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val His  
420 425 430

Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp Ala  
435 440 445

Met Leu Asp Met Met His Ser Glu Arg Lys Val Asp Val Tyr Gly Phe  
450 455 460

Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp Met  
465 470 475 480

Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu His Tyr Leu Tyr Gly

485	490	495
Asp Thr Glu Leu Glu Val Thr Ser Leu Glu Thr His Leu Gln Lys Ile 500	505	510
Tyr Asn Lys Ile Pro Gly Thr Ser Asn Asn Gly Leu Glu Glu Glu Phe 515	520	525
Lys Lys Leu Thr Ser Ile Lys Ile Gln Asn Asp Lys Met Arg Thr Gly 530	535	540
Asn Leu Pro Ala Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro 545	550	555
Tyr Glu Phe Asn Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn 565	570	575
Thr Asp Tyr Val Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp 580	585	590
Ser Tyr Ile Ala Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe 595	600	605
Trp Arg Met Ile Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr 610	615	620
Glu Leu Glu Glu Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser 625	630	635
Asp Gly Leu Val Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu 645	650	655
Glu Glu Cys Glu Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr 660	665	670
Arg Glu Asn Lys Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp 675	680	685
Pro Glu Val Gly Ile Pro Ser Asp Gly Lys Gly Met Ile Asn Ile Ile 690	695	700
Ala Ala Val Gln Lys Gln Gln Gln Gln Ser Gly Asn His Pro Ile Thr 705	710	715
Val His Cys Ser Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu 725	730	735
Ser Thr Val Leu Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe 740	745	750
Gln Thr Val Lys Ser Leu Arg Leu Gln Arg Pro His Met Val Gln Thr 755	760	765
Leu Glu Gln Tyr Glu Phe Cys Tyr Lys Val Val Gln Glu Tyr Ile Asp 770	775	780
Ala Phe Ser Asp Tyr Ala Asn Phe Lys 785	790	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGC GAGTGAGGCG CTGACAGGGA CTCGCGGGG CATCTTGCAC AGACCCCTGG	60
ACCACGCCGC CATCGCAGCC TCCAGCCCAG TCCTCTCTCT GCCGCTTCTC CTCGCCATGG	120
AGGCCGCCGA CCGCCGTCCG CGGGCTTCGA GCAGCGGACC GGGCCGGGCT GACCCCATGT	180
GGGCCGAGAG CCCGGTCQTG AGGCGGAGCT GCCGTGCGCG TCCCCGCGG TCCGCCCCCA	240
GCGCCGGGCT CGGTGAGCAT GGATTCTCTG TTCATTCTTG TCCTGTTTGG CAGTGGTCTA	300
ATACATGTTA GTGCCAACAA TGCTACTACA GTTTCACCTT CTTTAGGAAC GACAAGATTA	360
ATTAAACAT CAACAACAGA ATTGGCTAAG GAAGAGAATA AAACCTCAA TTCAACCTCT	420
TCAGTAATTT CTCTTTCTGT GGCACCAACA TTCAGCCCAA ACCTGACTCT GGAGCCCACC	480
TATGTGACTA CTGTTAATTC TTCACACTCT GACAATGGGA CCAGGAGGGC AGCCAGCAGC	540
GAATCTGGAG GCACTACCAT TTCCCCGAAC GGAAGCTGGC TTATTGAGAA CCAGTTCAGC	600
GATGCCATAA CAGAACCCTG GGAGGGGAAC TCCAGCACTG CAGCAACCAC TCCAGAAACC	660
TTCCCCCGG CAGATGAGAC ACCAATTATT GCGGTGATGG TGGCCCTGTC CTCTCTGCTA	720
GTAATCGTGT TTATTATCAT AGTTCGTAC ATGTTAAGGT TTAAGAAATA CAAGCAAGCT	780
GGGAGTCATT CCAACTCTTT CCGCCTGTCA AATGGCCGCA CGGAGGATGT GGAGCCCCAA	840
AGTGTAACCAC TTCTGGCCAG GTCCCCGAGC ACCAACAGGA AGTACCCACC ACTGCCTGTG	900
GACAAGCTGG AAGAGGAGAT TAACCGGAGA ATGGCTGATG ACAATAAGCT CTTCAGAGAA	960
GAATTCAACG CTCTCCCTGC TTGTCCTATC CAGGCCACCT GTGAGGCTGC CTCCAAGGAA	1020
GAAAACAAGG AAAAAACCG CTATGTAAAC ATCCTGCCCT ATGACCACTC TAGAGTGCAC	1080
CTGACACCTG TTGAAGGGGT CCCAGATTCT GATTACATCA ACGCTTCATT CATTAAATGGC	1140
TACCAGGAAA AGAACAAATT CATCGCTGCA CAAGGACCAA AAGAAGAAAC AGTGAATGAC	1200
TTCTGGAGAA TGATATGGGA ACAAAACACA GCTACTATTG TCATGGTGAC CAACCTGAAG	1260
GAGAGAAAGG AGTGTAATG TGCCAATAC TGGCCAGACC AAGGCTGCTG GACCTATGGG	1320
AATGTCCGTG TGTCTGTGCA GGATGTGACT GTTCTGGTGG ACTACACAGT ACGGAAATTC	1380
TCGATCCAGC AGGTGGGCGA CGTGACCAAC AGGAAACCAC AGCGCCTCAT CACTCAGTTC	1440
CACTTCACCA GCTGGCCAGA CTTTGGGGTG CCTTTCACCC CAATTGGCAT GCTCAAGTTC	1500
CTCAAGAAGG TGAAGGCCTG TAACCCTCAG TACGCAGGGG CTATCGTGGT CCACTGCAGT	1560
GCAGGTGTAG GGCGCACTGG CACCTTTGTT GTCATCGATG CCATGCTGGA CATGATGCAT	1620
TCGGAGCGCA AAGTGGATGT ATATGGGTTT GTGAGCCGGA TCCGGGCCCA GCGCTGCCAG	1680
ATGGTACAGA CAGACATGCA GTACGTCTTC ATATACCAGG CCCTTCTGGA GCATTATCTG	1740
TATGGGGACA CAGAACTGGA AGTGACTTCT CTAGAAACCC ACCTACAAA AATTTATAAC	1800
AAGATCCCAG GGACTAGCAA CAACGGGTTA GAGGAGGAGT TTAAGAAATT AACTTCAATC	1860
AAAATCCAGA ATGACAAGAT GCGCACGGGA AACCTTCCAG CCAACATGAA GAAGAACCGG	1920



GTTTTACAGA TCATTCCATA TGAATTTAAC AGAGTGATCA TTCCAGTCAA ACGAGGCGAA	1980
GAGAACACAG ACTATGTGAA CGCATCCTTC ATTGATGGAT ACCGGCAGAA AGACTCCTAC	2040
ATTGCCAGCC AGGGCCCTCT TCTCCACACG ATTGAGGACT TCTGGCGAAT GATCTGGGAG	2100
TGGAAGTCCT GTTCTATCGT AATGCTGACA GAACTGGAAG AGAGAGGCCA GGAGAAGTGT	2160
CCCCAGTACT GGCCATCTGA TGGCCTGGTG TCCTACGGAG ACATCACAGT TGAGCTGAAG	2220
AAGGAGGAGG AATGTGAAAG CTACACTGTC CGAGACCTCC TGGTCACCAA CACCAGGGAG	2280
AACAAGAGTC GGCAAATCCG GCAGTTCCAC TTCCACGGCT GGCCTGAGGT GGGCATCCCC	2340
AGCGACGGCA AGGGCATGAT CAACATCATT GCAGCAGTGC AGAAGCAGCA GCAGCAGTCG	2400
GGGAACCATC CCATCACTGT GCACTGCAGT GCCGGGGCAG GACGGACAGG AACCTTCTGT	2460
GCCTTGAGCA CAGTCCTGGA ACGTGTGAAA GCAGAAGGAA TTTTAGATGT CTTCCAAACT	2520
GTCAAGAGCC TCGGGCTGCA GAGGCCACAC ATGGTCCAGA CACTGGAACA GTATGAATTC	2580
TGCTACAAGG TGGTACAGGA ATACATTGAC GCCTTTTCAG ATTATGCCAA CTTCAAGTGA	2640
CAGGTGACAA GGCCACAGA CAGGAGAATT GCCTTTAATA TTTTGTATA TTCTGTTTTT	2700
GTTAATATAC CAAAAATTGT ATATATCTTA TAACTGTTTT AGAAATGGCA CATAGGCTTC	2760
TATTACCTGT TAGATGGAGA TTTTGTATGT AAATGTGTTA GCACTGATAG TCCTTTTCCA	2820
GTGTTTTATT GGGAAATTAA TAGTGTGATA TTTGGGTTGA TATAATGAAT TC	2872

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro	Tyr	Asp	Tyr	Asn	1	5	10	15
Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly	Ser	Asn	Tyr	Ile	20	25	30	
Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg	Lys	Tyr	Ile	Ala	35	40	45	
Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe	Trp	Arg	Met	Ile	50	55	60	
Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val	Thr	Arg	Cys	Glu	Glu	65	70	75	80
Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser	Met	Glu	Glu	Gly	85	90	95	
Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn	Gln	His	Lys	Arg	100	105	110	
Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val	Asn	Lys	Lys	Glu				

115	120	125
Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr Ser Trp Pro		
130	135	140
Asp His Gly Val Pro Glu Asp Pro His Leu Leu Lys Leu Arg Arg		
145	150	155
Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile Val Val His		
165	170	175
Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly Ile Asp Ala		
180	185	190
Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr Gly Tyr		
195	200	205
Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln Val Glu Ala		
210	215	220
Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser		
1	5	10
Arg Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile		
20	25	30
Asn Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala		
35	40	45
Ala Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile		
50	55	60
Trp Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu		
65	70	75
Arg Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Glu Trp		
85	90	95
Thr Tyr Gly Asn Ile Arg Val Ser Val Glu Asp Val Thr Val Leu Val		
100	105	110
Asp Tyr Thr Val Arg Lys Phe Cys Ile Gln Gln Val Gly Asp Met Thr		
115	120	125
Asn Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp		
130	135	140
Pro Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu		
145	150	155
Lys Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val		

165	170	175
His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp		
180	185	190
Ala Met Leu Asp Met Met His Thr Glu Arg Lys Val Asp Val Tyr Gly		
195	200	205
Phe Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp		
210	215	220
Met Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Lys His Lys Asn Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser  
1 5 10 15

Arg Val Lys Leu Ala Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp  
20 25 30

Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala Tyr  
35 40 45

Ile Ala Ala Gln Gly Pro Leu Lys Ser Thr Ala Glu Asp Phe Trp Arg  
50 55 60

Met Ile Trp Glu His Asn Val Glu Val Ile Val Met Ile Thr Asn Leu  
65 70 75 80

Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly  
85 90 95

Ser Glu Glu Tyr Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val  
100 105 110

Leu Ala Tyr Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile  
115 120 125

Lys Lys Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln  
130 135 140

Tyr His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu  
145 150 155 160

Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His Ala  
165 170 175

Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly  
180 185 190

Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln His Glu Gly  
195 200 205

Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg Ser Gln Arg Asn

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

[illegible]

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: /label= Xaa  
/note= "For the Consensus Sequence, Xaa = Lack of Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Asn Lys His Lys Asn Arg Tyr Xaa Asn Ile Leu Xaa Tyr Asp His Ser
1          5          10          15
Arg Val Lys Leu Xaa Xaa Leu Xaa Xaa Lys Xaa Xaa Lys Xaa Ser Asp
20          25          30
Tyr Ile Asn Ala Xaa Tyr Xaa Asp Gly Tyr Asn Glu Pro Lys Xaa Tyr
35          40          45
Ile Ala Ala Gln Gly Pro Leu Lys Xaa Thr Val Glu Asp Phe Trp Arg
50          55          60
Met Ile Trp Glu Gln Asn Thr Xaa Val Ile Val Met Xaa Thr Asn Leu
65          70          75          80
Val Glu Lys Gly Arg Arg Lys Cys Xaa Gln Tyr Trp Pro Xaa Xaa Gly
85          90          95
Ser Glu Xaa Tyr Gly Asn Ile Xaa Val Thr Val Lys Xaa Val Xaa Val
100         105         110
Leu Ala Xaa Xaa Asp Tyr Thr Val Arg Lys Phe Xaa Xaa Arg Asn Thr
115         120         125
Lys Ile Xaa Lys Xaa Gly Xaa Lys Xaa Xaa Xaa Lys Gly Arg Xaa Xaa
130         135         140
Gly Arg Val Val Thr Gln Tyr His Xaa Thr Xaa Trp Pro Asp Met Gly
145         150         155         160
Val Pro Glu Tyr Pro Leu Pro Val Leu Xaa Phe Val Arg Xaa Val Xaa
165         170         175
Ala Ala Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Val Val His Cys Ser Ala
180         185         190
Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Ile Asp Xaa Met Leu Gln
195         200         205
Gln Ile Xaa Xaa Glu Xaa Xaa Val Xaa Val Tyr Gly Phe Xaa Lys His
210         215         220
Ile Arg Xaa Gln Arg Xaa Tyr Xaa Val Gln Thr Glu Glu Gln Tyr Xaa
225         230         235         240
Phe Ile His Xaa Ala Leu Xaa Glu
245

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Asn Lys Ser Lys Asn Arg Asn Ser Asn Val Ile Pro Tyr Asp Tyr Asn
1           5           10           15
Arg Val Pro Leu Lys His Glu Leu Glu Met Ser Lys Glu Ser Glu His
20           25           30
Asp Ser Asp Glu Ser Ser Asp Asp Asp Ser Asp Ser Glu Glu Pro Ser
35           40           45
Lys Tyr Ile Asn Ala Ser Phe Ile Met Ser Tyr Trp Lys Pro Glu Val
50           55           60
Met Ile Ala Ala Gln Gly Pro Leu Lys Glu Thr Ile Gly Asp Phe Trp
65           70           75           80
Gln Met Ile Phe Gln Arg Lys Val Lys Val Ile Val Met Leu Thr Glu
85           90           95
Leu Lys His Gly Asp Gln Glu Ile Cys Ala Gln Tyr Trp Gly Glu Gly
100          105          110
Lys Gln Thr Tyr Gly Asp Ile Glu Val Asp Leu Lys Asp Thr Asp Lys
115          120          125
Ser Ser Thr Tyr Thr Leu Arg Val Phe Glu Leu Arg His Ser Lys Arg
130          135          140
Lys Asp Ser Arg Thr Val Tyr Gln Tyr Gln Tyr Thr Asn Trp Ser Val
145          150          155          160
Glu Gln Leu Pro Ala Glu Pro Lys Glu Leu Ile Ser Met Ile Gln Val
165          170          175
Val Lys Gln Lys Leu Pro Gln Lys Asn Ser Ser Glu Gly Asn Lys His
180          185          190
His Lys Ser Thr Pro Leu Leu Ile His Cys Arg Asp Gly Ser Gln Gln
195          200          205
Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu Leu Glu Ser Ala Glu Thr
210          215          220
Glu Glu Val Val Asp Ile Phe Gln Val Val Lys Ala Leu Arg Lys Ala
225          230          235          240
Arg Pro Gly Met Val Ser Thr Phe Glu Gln Tyr Gln Phe Leu Tyr Asp
245          250          255
Val Ile Ala Ser
260

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn
1      5      10
Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val
20     25     30
Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala
35     40     45
Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile
50     55     60
Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu
65     70     75     80
Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val
85     90     95
Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu
100    105    110
Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys
115    120    125
Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly
130    135    140
Ile Pro Ser Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln
145    150    155    160
Lys Gln Gln Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser
165    170    175
Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu
180    185    190
Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys
195    200    205
Ser Leu Ala Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr
210    215    220
Glu Phe Cys Tyr Lys Val Val Gln Glu
225    230

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn Arg Glu Lys Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser  
 1 5 10 15  
 Arg Val Gly Ile Ser Ser Leu Ser Gly Glu Gly Thr Asp Tyr Ile Asn  
 20 25 30  
 Ala Ser Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr  
 35 40 45  
 Gln His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile Trp  
 50 55 60  
 Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln Asn Met  
 65 70 75 80  
 Ala Glu Asp Glu Phe Val Tyr Trp Pro Asn Lys Asp Glu Pro Ile Asn  
 85 90 95  
 Cys Glu Ser Phe Lys Val Thr Leu Met Ala Glu Glu His Lys Cys Leu  
 100 105 110  
 Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe Ile Leu Glu Ala Thr  
 115 120 125  
 Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys Trp  
 130 135 140  
 Pro Asn Pro Asp Ser Pro Ile Ser Lys Thr Phe Glu Leu Ile Ser Val  
 145 150 155 160  
 Ile Lys Glu Glu Ala Ala Asn Arg Asp Gly Pro Met Ile Val His Asp  
 165 170 175  
 Glu His Gly Gly Val Thr Ala Gly Thr Phe Cys Ala Leu Thr Thr Leu  
 180 185 190  
 Met His Gln Leu Glu Lys Glu Asn Ser Val Asp Val Tyr Gln Val Ala  
 195 200 205  
 Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Ala Asp Ile Glu Gln  
 210 215 220  
 Tyr Gln Phe Leu Tyr Lys Val Ile Leu Ser  
 225 230

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Val Val Pro Ser Glu Arg Ala  
 1 5 10 15  
 Arg Val Gly Leu Ala Pro Leu Pro Gly Met Lys Gly Thr Asp Tyr Ile  
 20 25 30  
 Asn Ala Ser Tyr Ile Met Gly Tyr Arg Ser Asn Glu Phe Ile Ile  
 35 40 45



Thr Gln His Pro Leu Pro His Thr Thr Lys Asp Phe Trp Arg Met Ile  
50 55 60

Trp Asp His Asn Ala Gln Ile Ile Val Met Leu Pro Asp Asn Gln Ser  
65 70 75 80

Leu Ala Glu Asp Glu Phe Val Tyr Trp Pro Ser Arg Glu Glu Ser Met  
85 90 95

Asn Cys Glu Ala Phe Thr Val Thr Leu Ile Ser Lys Asp Arg Leu Cys  
100 105 110

Leu Ser Asn Glu Glu Gln Ile Ile Ile His Asp Phe Ile Leu Glu Ala  
115 120 125

Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys  
130 135 140

Trp Pro Asn Pro Asp Ala Pro Ile Ser Ser Thr Phe Glu Leu Ile Asn  
145 150 155 160

Val Ile Lys Glu Glu Ala Leu Thr Arg Asp Gly Pro Thr Ile Val His  
165 170 175

Asp Glu Tyr Gly Ala Val Ser Ala Gly Met Leu Cys Ala Leu Thr Thr  
180 185 190

Leu Ser Gln Gln Leu Glu Asn Glu Asn Ala Val Asp Val Phe Gln Val  
195 200 205

Ala Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Thr Asp Ile Glu  
210 215 220

Gln Tyr Gln Phe Ile Tyr Lys Ala Arg Leu Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 280 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites  
(B) LOCATION: 1..280  
(D) OTHER INFORMATION: /label= Xaa  
/note= "For the Consensus Sequence, Xaa = Lack of Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Xaa Ile Pro Tyr Glu Arg Asn  
1 5 10 15

Arg Val Gly Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Glu Glu Gly Thr  
35 40 45

Asp Tyr Ile Asn Ala Ser Xaa Ile Met Gly Tyr Tyr Gln Ser Asn Glu  
50 55 60

Phe Ile Xaa Thr Gln Xaa Pro Leu Leu His Thr Ile Lys Asp Phe Trp  
 65 70 75 80  
 Arg Met Ile Trp Asp His Xaa Asn Ala Gln Ile Val Met Leu Xaa Xaa  
 85 90 95  
 Xaa Gln Xaa Xaa Ala Glu Xaa Glu Xaa Xaa Gln Tyr Trp Pro Ser Xaa  
 100 105 110  
 Gly Xaa Xaa Xaa Tyr Gly Asp Xaa Xaa Val Xaa Leu Lys Xaa Xaa Xaa  
 115 120 125  
 Asn Cys Glu Ser Xaa Thr Val Thr Xaa Xaa Xaa Glu Xaa Arg Xaa Cys  
 130 135 140  
 Leu Ser Asn Glu Xaa Arg Xaa Ile Ile Gln Asp Phe Ile Leu Glu Ala  
 145 150 155 160  
 Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys  
 165 170 175  
 Trp Pro Asn Pro Asp Xaa Pro Ile Ser Xaa Thr Xaa Glu Leu Ile Ser  
 180 185 190  
 Val Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Glu Glu Ala  
 195 200 205  
 Xaa Asn Arg Xaa Xaa Xaa Asp Gly Pro Xaa Ile Val His Xaa Glu Xaa  
 210 215 220  
 Gly Ala Val Xaa Xaa Gly Thr Phe Cys Ala Leu Thr Thr Leu Leu Glu  
 225 230 235 240  
 Gln Leu Glu Xaa Glu Asn Xaa Val Asp Val Phe Gln Val Xaa Lys Met  
 245 250 255  
 Xaa Asn Leu Met Arg Pro Gly Xaa Xaa Xaa Xaa Ile Glu Gln Tyr Gln  
 260 265 270  
 Phe Leu Tyr Lys Val Ile Leu Ser  
 275 280

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